

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: March 2, 2002, 23:35:23 ; Search time 2023.3 Seconds  
(without alignments)  
8316.672 Million cell updates/sec  
Title: US-08-989-881-1  
Perfect score: 1020  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_on.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_sts.\*
- 27: em\_sy.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htgo\_hum.\*
- 31: em\_htgo\_inv.\*
- 32: em\_htgo\_rod.\*
- 33: em\_htg\_hum.\*
- 34: em\_htg\_inv.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	652	63.9	1842	8	ATHCDPKA	D21805 Arabidopsis
3	526.8	51.6	115721	8	F25A4	AC008263 Arabidopsis
4	449	44.0	1998	8	ATU31836	U31836 Arabidopsis
5	449	44.0	2115	8	AF361634	AF361634 Arabidopsis
6	448.4	44.0	2087	6	AX077698	AX077698 Sequence
7	448.4	44.0	2162	6	AX077694	AX077694 Sequence
8	437.2	42.9	1967	6	AX077712	AX077712 Sequence
9	437.2	42.9	1967	8	AF035944	AF035944 Fragaria
10	432.4	42.4	1726	6	AX077695	AX077695 Sequence
11	432.4	42.4	1896	8	ATU20624	U20624 Arabidopsis
12	421.4	41.3	2313	8	AF276999	AF276999 Funaria h
13	384.4	37.7	108767	8	AC011809	AC011809 Arabidopsis
14	367.2	36.0	1647	6	AX077713	AX077713 Sequence
15	367.2	36.0	1647	6	AX077714	AX077714 Sequence
16	367.2	36.0	1647	8	AB017516	AB017516 Marchanti
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19	358.4	35.1	2363	6	AX077716	AX077716 Sequence
20	358.4	35.1	2363	8	AF090835	AF090835 Mesembrya
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22	356.2	34.9	1858	8	ATHATCDPK	D28582 Arabidopsis
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26	346.2	33.9	1747	8	ATHCDPKB	D21806 Arabidopsis
27	340.6	33.4	2243	8	TR082087	U82087 Tortula rur
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ALIGNMENTS

RESULT 1

ATU73610

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

ATU73610 822 bp mRNA PLN 02-DEC-1999  
Arabidopsis thaliana ATCDPK1a (cpk1a) mRNA, partial cds.

U73610 GI:6502506

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 822)

Sheen, J.

Ca2+-dependent protein kinases and stress signal transduction in plants

Unpublished

2 (bases 1 to 822)

Sheen, J.

Direct Submission



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DEFINITION Arabidopsis thaliana chromosome 1 BAC F25A4 sequence, complete  
ACCESSION AC008263  
VERSION AC008263.2 GI:5868932  
KEYWORDS HTG  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 115721)  
REFERENCE Vysotskai,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,

Lee, J.M., Li, J., Gonzalez, A., Liu, A., Liu, K., Vaysberg, M., Sakano, H., Chin, C., Choi, E., Chou, J., Altafi, H., Araujo, R., Brooks, S., Ruehler, E., Chao, Q., Conn, L., Conway, A.B., Dunn, P., Hansen, N., Hwang, B., Huizar, L., Khan, S., Kim, C., Palm, C., Rowley, D., Shinn, P., Walker, M., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A.  
Arabidopsis thaliana chromosome 1 BAC F25A4 sequence  
Unpublished  
2 (bases 1 to 115721)  
Theologis, A.  
Direct Submission  
Submitted (31-JUL-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
3 (bases 1 to 115721)  
Theologis, A.  
Direct Submission  
Submitted (10-SEP-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
4 (bases 1 to 115721)  
Theologis, A.  
Direct Submission  
Submitted (15-SEP-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
On Sep 10, 1999 this sequence version replaced gi:5668776.  
The sequence of BAC F25A4 from Arabidopsis thaliana chromosome 1.  
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RESULT 4
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DEFINITION Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 7 (CPK7) mRNA, complete cds.
ACCESSION U31836
VERSION U31836.1 GI:1399276
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL 1 (bases 1 to 1998)
AUTHORS Hrabak, E.M., Dickmann, L.J., Satterlee, J.S. and Sussman, M.R.
TITLE The calmodulin-domain protein kinase (CDPK) gene family of
JOURNAL Arabidopsis thaliana contains at least twelve members
REFERENCE Unpublished (1995)
AUTHORS Hrabak, E.M.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1995) Estelle Hrabak, Horticulture, University of
Wiscconsin, 1575 Madison, WI 53706, USA
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RESULT 6  
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 DEFINITION Sequence 5 from Patent WO0107592.  
 ACCESSION AX077698  
 VERSION AX077698.1 GI:13122073  
 KEYWORDS Arabidopsis sp.  
 SOURCE Arabidopsis sp.  
 ORGANISM Arabidopsis sp.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 2087)  
 AUTHORS Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.  
 TITLE Herbicide resistant plants and methods for the production thereof  
 JOURNAL Patent: WO 0107592-A 5 01-FEB-2001;  
 ZENCA LIMITED (GB)  
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 DEFINITION Sequence 1 from Patent WO0107592.  
 ACCESSION AX077694  
 VERSION AX077694.1 GI:13122069  
 KEYWORDS synthetic construct.  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequence.  
 1 (bases 1 to 2162)  
 AUTHORS Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.  
 TITLE Herbicide resistant plants and methods for the production thereof  
 JOURNAL Patent: WO 0107592-A 1 01-FEB-2001;  
 ZENCA LIMITED (GB)  
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 BASE COUNT 601 a 409 c 522 g 630 t  
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DEFINITION AX077712
VERSION AX077712.1 GI:13122087
KEYWORDS
SOURCE
ORGANISM
Fragaria x ananassa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.
1 (bases 1 to 1967)
Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.
Herbicide resistant plants and methods for the production thereof
Patent: WO 0107592-A 19 01-FEB-2001;
ZENECA LIMITED (GB)
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LOCUS Fragaria x ananassa calcium-dependent protein kinase (MAX17) mRNA,
DEFINITION complete cds.
ACCESSION AF035944
VERSION AF035944.1 GI:2665889
KEYWORDS
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Fragaria x ananassa.
Fragaria x ananassa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Fragaria.
1 (bases 1 to 1967)
Llop-Tous, J., Dominguez-Puigjaner, E. and Vendrell, M.
Submitted (26-NOV-1997) Agrobiologia, CSIC, Jordi Girona 18-26,
Barcelona 08034, Spain
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LOCUS Sequence 2 from Patent WO0107592.
DEFINITION AX077695
ACCESSION AX077695
VERSION AX077695.1 GI:13122070
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SOURCE Arabidopsis sp.
ORGANISM Arabidopsis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 2 01-FEB-2001;
ZENECA LIMITED (GB)
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## JOURNAL

Submitted (22-JAN-2000) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

## COMMENT

On Dec 15, 1999 this sequence version replaced gi:6041764.

e-mail for correspondence: arab@sequence.stanford.edu  
Genes with similarity to proteins in the databases are described  
as 'putative', '-like', or 'similar to'. Genes that have EST  
similarity but no significant protein similarity are described as  
'unknown proteins'. Genes that are annotated based only on gene  
prediction software are described as 'hypothetical proteins'. The  
software programs used to predict genes include: Grail  
(Informatics Group, Oak Ridge National Laboratory,  
<http://complib.ornl.gov/section/index.html>), GENSCAN (Chris Burge,  
<http://genome.stanford.edu/~chris/GENSCANW.html>), Fexa (V. Solovyev  
& A. Salamov, Sanger Centre, <http://genomic.sanger.ac.uk/>), and  
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of  
Denmark, <http://www.cbs.dtu.dk/NetPlantGene.html>).

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REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta;		
AUTHORS	Marchantiophyta; Marchantiales; Marchantiaceae; Marchantia.		
TITLE	1 (bases 1 to 1647)		
JOURNAL	Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.		
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ACCESSION AX077714
VERSION AX077714.1 GI:13122089
KEYWORDS liverwort.
SOURCE Marchantia polymorpha
ORGANISM Marchantia polymorpha
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
AUTHORS Marchantiophyta; Marchantiales; Marchantiaceae; Marchantia.
TITLE Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
JOURNAL Herbicide resistant plants and methods for the production thereof
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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5	437.2	42.9	1967	22	AAF74280 Strawberry calciu
6	432.4	42.4	1726	22	AAF74263 Arabidopsis calciu
7	367.2	36.0	1847	22	AAF74281 Liverwort calciu
8	367.2	36.0	1847	22	AAF74282 Common ice plant c
9	358.4	35.1	2363	22	AAF74284 Rice calciu depen
10	355.4	34.8	2040	22	AAF74278 Arabidopsis thalia
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14	332.8	32.5	2306	22	AAF74272
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KW	fruit; ornamental; vegetable; cereal; field crops; ds.
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PA	(GEHO ) GEN HOSPITAL CORP.
XX	
PI	Sheen J;
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DR	WPI; 1998-348509/30.

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Tobacco homolog of  
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Carrot calcium dep  
Rice calcium depen  
Vigna radiata calc  
Arabidopsis thalia  
Sweet potato calci  
Protein Kinase cDN  
Cucurbita pepo cal  
Soybean calcium de  
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Potato calcium dep  
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Plasmodium falcipa  
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Db 1078 tcagacaaatgttagagcctgattccaaagcgtcggtcactgcaagcaagtgcttgagc 1137
QY 893 acccttgatcacagaatcaagaagaaagatcaagcctt 930
Db 1138 accatgattcacaagcaagaagatcccaatggt 1175

RESULT 4
ID AAC47633 standard; DNA; 1836 BP.
AC AAC47633;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54543.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN BP1033405-A2.
PD
PF 06-SEP-2000.
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 28-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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XX 01-FEB-2001.
PD
XX
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
XX 27-JUL-1999; 99GB-0017642.
XX
XX (ZENE ) ZENECA LTD.
PA
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
XX WPI; 2001-168549/17.
DR
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX
XX Claim 18; Page 41; 50pp; English.
PS
XX
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX
XX Sequence 1967 BP; 572 A; 334 C; 500 G; 561 T; 0 other;
SQ

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Query Match 42.9%; Score 437.2; DB 22; Length 1967;  
 Best Local Similarity 71.2%; Pred. No. 2.2e-123;  
 Matches 577; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

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QY 109 actcagatcagcgacaaagtacattcttagagagagaaactcgtcgcgggaattcggaaac 168
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
163 actgaatcgagcagacttagcagctggcgcgagagctcggcgcgagagtgaggatt 222
QY 169 acgtatctttacagatagagagactcgtgaagcttttagcttgcacaaatcattccaa 228
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
223 acgtactctgtactgacaaagccaccacagagaaactacgcttgcaaatcagatcgag 282
QY 229 agaagctccgaacgcgcgtgatgtggaagacgtccgtggaagtcaacgatcatgtca 288
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
283 cagaactagagagcgctgtgattgaagtgaagctgagaggggaagttagatcatgaag 342
QY 289 actttaccggaaccccaacacgttgtgaaacttaagcgaacttatgagataacagagacc 348
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
343 cacttgctaagcatcccaatttgtgagcttgaagataccttacgaggtgataatgct 402
QY 349 gtgcatttgtgagagacttgttgaaggaggtgagctttttgctcggagattgtgcaaga 408
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
403 gtccatttgttggagctctgtgagggcggtgagctttttgctcggagctgtctagg 462
QY 409 ggacattatcacagagcgtgcggcggtacgcgcggaacgagatcgcggagttgtgagg 468
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
463 ggacattacactgagcgtgctgctgctgctgctgctgctgctgctgctgctgctgct 522
QY 469 atgtgtcatgcaatggtgttatgcatagagatttgaagcctgagaatttctgtttgct 528
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
523 atgtgccacaagcatggtgtgagccaccggatcttaaacctgagaacttttgttgca 582
QY 529 aacaagaagagagaattctgcaactaagcgtattgatttggtttatctgttctctaaa 588
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
583 aacaagaagaacagcgccttgaaggcaattgatttgggtgtcaggttctttaaag 642
QY 589 cctggagagaggtttacagagatttgttgaagtccttattatggtcctcagaagtgttg 648
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
643 cctggtgaaagattcagtgaaattgttgaagtccttattatggtcctcagaagtgttg 702
QY 649 aagagaattatggaacagaggttgatgtgtgagtgctgaggtatctctacatttg 708
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
703 agacgcaattatggtcctgaaagtgtatgtgagtgctgaggtatctctacatttg 762
QY 709 ctttgtggttctcctcgttttgggcagagactgaacaaagggtgtggtccttgccatttg 766

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DB 763 ctttgtgtgttcgcgcttcttctgggcagaaactgaacaggaggtgcacaagcaattata 822
QY 769 agggaggtcttctgattttaagagagatccttggtcgcagatatcagagagcgcaagc 828
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
823 cgtctgtgttagattttaagaggagaccctggcctaagggtttctgataatgcacaaagac 882
QY 829 cttgtgaagcagatgtttgggaacctgattcaactaaagcgtttgactgctcagcaagttctt 888
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
883 cttgtgaaaaagatgcttgatcctgcaccggaagcgagggttacagctcagcaagttctt 942
QY 889 gatcaccccttggtatcacagaatgcaagaaa 918
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
943 gatcactctggttgcaaaatgcaagaga 972

```

## RESULT 6

AAAF74263

ID AAF74263 standard; DNA; 1726 BP.

AC AAF74263;

DT 04-MAY-2001 (first entry)

DE Arabidopsis calcium dependent protein kinase clone 15-1.

KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
 paraquat; diquat; crop production; ds.

OS Arabidopsis sp.

PN WO200107592-A2.

PD 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB02876.

XX 27-JUL-1999; 99GB-0017642.

XX (ZENE ) ZENECA LTD.

XX Holt CD, White AJ, Michael AJ, Osborn RW;

XX WPI; 2001-168549/17.

Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole -  
 Claim 17; Page 32; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Sequence 1726 BP; 518 A; 279 C; 449 G; 480 T; 0 other;

Query Match 42.4%; Score 432.4; DB 22; Length 1726;  
 Best Local Similarity 71.5%; Pred. No. 6e-122;  
 Matches 568; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

```

QY 124 aagtacattttagagagagaaactcgtcgcgggaattcggaaatcactgttctttgaca 183
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
60 atgtatgatctggcggtgaggttggtcgcggagagttggttacttacttactgtgcaact 119
QY 184 gatagagagactcgtgaagcttttagcttgcacaaatcactcctcagaagaagctccgaac 243
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 gatatacaaacggcgagagagatgctgcaagctctatatcaagaagaagcttagaaca 179
QY 244 gcgcgtgatgtggaagacgtccgctgctggaagtcacgatcatgtccaattitacgggaac 303

```



Sequence 2363 BP; 718 A; 435 C; 542 G; 668 T; 0 other;

Query Match	35.1%;	Score 358.4;	DB 22;	Length 2363;	
Best Local Similarity	64.7%;	Pred. No. 3e-99;			
Matches 533;	Conservative	0;	Mismatches 291;	Indels 0;	Gaps 0;

  

QY	125	agtaacatcttagagcagaaactcgctgcgcggcaattoggaatcaatcagctatctttgtacag	184
Db	589	actcacacttgggagagaaactgggtgagggtcaatttgggttaccatctctgtgcaatg	648
QY	185	atagagagactcgtgaagcttttagctttcaaatcaatctcaagaagaagctccgaaccg	244
Db	649	acaaaagaactggcaacaatatgcttgcgaagctcaatctcaagaagaagcttggacca	708
QY	245	cgtcgtatgtgaagacgtccgtctgtaagtcacgatcatgtcaactttaccgaaacacc	304
Db	709	aggctgatgaagatgatataaggagagagattcagatcatgcagcatagtagtgtaaac	768
QY	305	caaacgttgtgaacttaaacgcacttaaggataacgagacogtgcattctgtgatgg	364
Db	769	ctaacatttgggaatttaagggtgcttatgagataaaacatctgtgaactctgtgatgg	828
QY	365	agcttttgaaaggagtgtagcttttggctcggaatttggcaagagacattatacaagc	424
Db	829	agctttgtgctgtgggagttgtttgatagattattgtctaaagggcattatagtga	888
QY	425	gtgcgcgcgtaccgtcgcgagaaacgtgcgcggaagttgtgagagatgtgcatgtcaatg	484
Db	889	aggctgcgtccactatgttgaggagatgtttaattgtttcattgtgtcactattatgg	948
QY	485	gtgttatgcataagatattgaagctgagaattctctgtttgctaaacaagaagagaaatt	544
Db	949	gtgtgatgcataggatctgaagctgagaactcttgcctctcagacaagatgagaatt	1008
QY	545	ctgcacttaaggtctattgattttggtttatctgttctctttaaacctggagaggttta	604
Db	1009	ctcttggaaagccactgattttgggtgtctgtgtttattgaaagaaggtaaagtctaac	1068
QY	605	cagagattgttggaaagtccttatataatggtccagaagtggtgaagaagaattatggac	664
Db	1069	gggatatagtaggcagtgcttactactgcgctcgtgaggtattgcgtcgtaggtatggga	1128
QY	665	cagaggttgatgtgtgagtgctggagttatctctctacatcttgccttgcgtgtctc	724
Db	1129	aggagattgattgttgagtgctgagtgatgtgtacatcttactcaagtcggtgcccc	1188
QY	725	cgttttggcagagactgaacaaggtgtggtctcttgcacbtctgagggagttcttgatt	784
Db	1189	ccctttgggcgaagacggaaagggtatctttgatgtattttgcaggccattgatt	1248
QY	785	ttaagagagatccttggctgcagatatacagagagcgcaagaccctgttgaagcagatgt	844
Db	1249	tcgaaagcaaacatggccatcaattcaaatggtccaggaccctagtgaaaaaattgt	1308
QY	845	tggaaacctgattcaactaaagcgtttgactgctcagcagttcttgatcacaccttggat	904
Db	1309	tgacagaggtatcccaagaaacggattactgctgctcaagttcttggagcccatggctaa	1368
QY	905	agaatgcagaagaaagatcaagcttatcgataccgtcgacctc	948
Db	1369	gagatgtgaagcatcagacaagcccaatagacagtgctgtcttc	1412

  

RESULT	10
AAAF4278	
ID	AAAF4278 standard; DNA; 2040 BP.
XX	
AC	AAAF4278;
XX	
Dm	04-MAY-2001 (first entry)
XX	
DE	Rice calcium dependent protein kinase clone #2.
XX	

KW	Calcium dependent protein kinase; CDPK; herbicide resistance;
KW	paraquat; diquat; crop production; ds.
XX	
OS	Oryza sp.
XX	
PN	WO200107592-A2.
XX	
PD	01-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-GB02876.
XX	
PE	27-JUL-1999; 99GB-0017642.
XX	
PA	(ZENE ) ZENECA LTD.
XX	
PI	Holt CD, White AJ, Michael AJ, Osborn RW;
XX	
DR	WPI; 2001-168549/17.
XX	
PT	Producing herbicide resistance plants by inhibiting calcium dependent
PT	protein kinase in plants or by providing an intracellular vacuolar
PT	transporter capable of transporting agrochemical into plant vacuole -
XX	
PS	Claim 18; Page 40; 50pp; English.
XX	
CC	The present invention describes a method of producing plants which are
CC	resistant to the herbicides paraquat and diquat, involving inhibiting in
CC	the plants a calcium dependent protein kinase (CDPK) and selecting those
CC	plants which are resistant to the agrochemical of interest. This is
CC	useful in the production of crops with herbicide resistance.
XX	
SQ	Sequence 2040 BP; 586 A; 415 C; 513 G; 526 T; 0 other;

Query Match	34.8%;	Score 355.4;	DB 22;	Length 2040;	
Best Local Similarity	64.6%;	Pred. No. 2.3e-98;			
Matches 530;	Conservative	0;	Mismatches 291;	Indels	Gaps
QY 127	tacattcttagacgagaactcgtgcgcgcgcgaattcggaaatccacgtatctttgtacagat	186			
Db					
QY 425	tactcccttgaaagaaactcggaaagggcagtttgggtgacatacctgtgcacggag	484			
Db					
QY 187	adagagaactcgtgaagcctttagcttgcgaatcaatctccaaagagaagaactccgaacgcgc	246			
Db					
QY 485	atcgctagtgtlaagcagtagcttgcgaatccatctcgaacgcgaactgtgtgagaag	544			
Db					
QY 247	gtgatgtggaagacgtccgtctgtaagtacgatcatgtcaactttaccggaacaccca	306			
Db					
QY 545	gccacaaggaggacattcgcgcggagattcagatcatgcagcacctatctggacaaca	604			
Db					
QY 307	aacgttgtgaaacttaaaacgcacttatgagataaacagagacccgtgcattctgtgtatggag	365			
Db					
QY 605	aacattgcgagttccggggagacatacgaggaacagagcaatgtccatgtgttcattggag	664			
Db					
QY 367	ctttgtgaagagagtgagccttttggctcgagttgttgcgaaggagacattatcacagacgt	426			
Db					
QY 665	ctctgcgctgtgtgggagcgttttgatcggatcattgccaaagggcactactcagagcgt	724			
Db					
QY 427	gcgcgcgctccgcgcgagaacgatccgggaagctgtgaggatgtgtcatgtccaatggt	486			
Db					
QY 725	gcggctctacacctgcagggcagtgatgtgtcgaacattgccattttatggga	784			
Db					
QY 487	gttatgcatagagattggaagcctgagaattctctgttgcatacaagaaggagaattct	546			
Db					
QY 785	gtgatgcactgtgatttgaacccggagaaacttctacttgcaaccaaagaagagatgca	844			
Db					
QY 547	gcacttaagcctattgatttggtttatctgtctcttttaaacctgcagagaggtttaca	606			
Db					
QY 845	atgtccaaagccactgatttggctctcagtttctcattgagaagaagaaaatgtataga	904			
Db					
QY 607	gagattgttgaagtcctattatatagctccagaagtggttgaagagaattatgacca	666			
Db					
QY 905	gacattgttgaagtcctattatgtccctgaagtccttcggcggaattatgtgttaa	964			
Db					

RESULT_10	
AAAF74278	
ID	AAAF74278 standard; DNA; 2040 BP.
XX	
AC	AAAF74278;
XX	
DT	04-MAY-2001 (first entry)
XX	
XX	Rice calcium dependent protein kinase clone#2.
XX	

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QY 667 gaagtgatgtgtgagtgctgagtgatctcctacatcttctgtgtgtgtctctcgg 726
    ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 965 gagattgatgtgagtgagtcaggcggtattttgtacattctctcagtggtgtctctcca 1024
QY 727 ttttggcagactgaacaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 786
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1025 ttttggcagactgaacaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1084
QY 787 aagagagatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 846
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1085 gagagtcacccatgcccataatccgagtgctaaagacctgtttagaagaatgttg 1144
QY 847 gaactgtatcaactaaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 906
    || ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1145 acacaagatccaaagaagaattacttcggcccaagtcttccaacatcctcgtgtcaga 1204
QY 947 aatgcaaaagaagaagcaagctttatcataacgctgcgacct 947
    ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1205 gatgagaagcatcgcacaaacctattgacagcgtgtct 1245

RESULT 11
AAC48741
ID AAC48741 standard; DNA; 1392 bp.
XX
- AC AAC48741;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58595.
- KW
- KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
FN EP1033405-A2.
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 24-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
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QY 162 cgaatacagatctctgttacagatagagactcgtgaagcttttagcttgcaaatcaat 221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 222 ctccagagaagctccgaacccgctcgtatgtggaagcctcgtcgtggaagtcacgat 281
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 282 catgtcaactttaccggaacacccaaacgttgtaaaacttaagcgaacttatgagataa 341
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Db 444 atgcatcatttagctggcaccgtagtatcgtgacgattaaaggagcttatgaggactc 503

QY 342 cgagacgtgcactctgtgatgagctttgtgaagagagtgagcttttggctcgattgt 401
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QY 402 tcaagagagacattatacagagcgtgcgcggtcaccgtcgcgagaaactcgcggaagt 461
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QY 462 tgtgaggtatgtcatgtcaatgtgttatgcatagagatttgaagccttgagaatttctt 521
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RESULT 14
AAAF74272
ID AA74272 standard; DNA: 2306 BP.
XX
AC AA74272;
XX
DT 04-MAY-2001 (first entry)
XX
DE Maize calcium dependent protein kinase clone #2.
XX
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KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
XX Zea mays.
XX
XX WO200107592-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-GB02876.
XX
XX 27-JUL-1999; 99GB-0017642.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Holt CD, White AJ, Michael AJ, Osborn RW;
XX
XX WPI; 2001-168549/17.
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
XX protein kinase in plants or by providing an intracellular vacuolar
XX transporter capable of transporting agrochemical into plant vacuole
XX
XX Claim 18; Page 35-36; 50pp; English.
XX
XX The present invention describes a method of producing plants which are
XX resistant to the herbicides paraquat and diquat, involving inhibiting in
XX the plants a calcium dependent protein kinase (CDPK) and selecting those
XX plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX
XX Sequence 2306 BP; 590 A; 519 C; 611 G; 586 T; 0 other;
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Best Local Similarity 64.3%; Pred. No. 2e-91;
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QY 187 agagagactcgtgaagcttttagcttgcaaatcaatctccaagagaagaactccgaaccgc 246
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QY 427 gcggcgcctacgcctgcggaacacatgcgggaagttgtgaggtgtgtcatgtcaatggt 486
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QY 487 gttatgcatagagatttgaagcctgagaattctgtttgttcttaaacctgagagaggaattct 546
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 23:36:48 ; Search time 76.56 Seconds  
(without alignments)  
3017.340 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	226	22.2	4162	3	US-08-459-504B-26
4	226	22.2	4162	3	US-08-459-444-26
5	226	22.2	4165	1	US-07-951-715A-26
6	225.6	22.1	1349	1	US-07-951-715A-20
7	225.6	22.1	1349	2	US-08-459-448A-20
8	225.6	22.1	1349	3	US-08-459-595A-20
9	225.6	22.1	1349	3	US-08-459-504B-20
10	225.6	22.1	1349	3	US-08-459-444-20
11	219.8	21.5	2374	4	US-09-347-801-3
12	148.2	14.5	1400	1	US-08-464-164-1
13	148.2	14.5	1400	1	US-08-338-057-1
14	148.2	14.5	1400	2	US-08-668-416-1
15	136.6	13.4	1776	3	US-08-655-352-10
16	117	11.5	2514	3	US-08-655-352-1
17	97.4	9.5	498	4	US-09-347-801-7
18	84.6	8.3	5707	2	US-08-472-809B-8
19	83	8.1	270	1	US-08-181-629A-12
20	82.4	8.1	1282	2	US-08-878-989-12
21	82.4	8.1	1282	4	US-09-272-796-12
22	82	8.0	2027	3	US-08-930-996A-6
23	82	8.0	3198	4	US-08-842-306B-48
24	82	8.0	3198	4	US-08-838-973B-48
25	82	8.0	6345	2	US-08-472-809B-7
26	81.4	8.0	329	1	US-08-703-809-9
27	81.4	8.0	329	1	US-08-703-808-9

C 28	81.4	8.0	329	2	US-08-703-807-9	Sequence 9, Appli
C 29	81.4	8.0	329	2	US-08-747-108A-9	Sequence 9, Appli
C 30	81.4	8.0	329	3	US-09-211-631-9	Sequence 9, Appli
C 31	81.4	8.0	329	3	US-09-265-628-9	Sequence 9, Appli
C 32	81.4	8.0	329	4	US-09-532-803-3	Sequence 3, Appli
C 33	81.2	8.0	4164	1	US-08-204-675-1	Sequence 1, Appli
C 34	81.2	8.0	4164	2	US-08-660-754-1	Sequence 1, Appli
C 35	81.2	8.0	4164	2	US-08-796-364-1	Sequence 1, Appli
C 36	81.2	8.0	4164	5	PCT-US95-02520-1	Sequence 1, Appli
C 37	81.2	8.0	4933	1	US-08-204-675-1	Sequence 1, Appli
C 38	81.2	8.0	4933	2	US-08-660-754-2	Sequence 2, Appli
C 39	81.2	8.0	4933	2	US-08-796-364-2	Sequence 2, Appli
C 40	81.2	8.0	4933	5	PCT-US95-02520-2	Sequence 2, Appli
C 41	79.8	7.6	11233	4	US-08-980-832-27	Sequence 27, Appli
C 42	77.4	7.6	380	2	US-08-735-609-5	Sequence 5, Appli
C 43	77.4	7.6	380	2	US-08-735-609-5	Sequence 5, Appli
C 44	77.4	7.6	380	3	US-09-315-372-5	Sequence 5, Appli
C 45	77.4	7.6	380	3	US-09-244-752-5	Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-08-459-448A-26  
; Sequence 26, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5859336artis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,448A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40403

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REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
- INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
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FEATURE:
NAME/KEY: intron
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FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26

Query Match 22.2%; Score 226; DB 2; Length 4162;
Best Local Similarity 60.4%; Pred. No. 5.1e-61;
Matches 373; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

QY 119 gqacaagtacatcttagacgagaaactcggtcgcgcggaatttcggaatacagtatcttt 178
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QY 179 gtacagatagagagactcgtgaagcttttagcttgcaaatcaatctccaagagaaaagctcc 238
Db 1809 GCACGACCGGAGAGCGCGGAGAACTGCGTGAAGACGATCGGAAGCGGAAGCTGG 1868
QY 239 gaaccgctcgatgtggaagacgtccgtcgtaagtcaagatcagatcatcgaactttaccgg 298
Db 1869 CGGCCAGGAGGAGCTGGACGAGTGGGGGGAGGTGCAGATCATGCACCACTCTCCG 1928
QY 299 aaaccccaacgttgtgaacactaaagcagacttatgagataaacgagacggtgcatttg 358
Db 1929 GCAGGCCAACGTGTGGCTCCGGGGGCGGTACGAGGACAAAGCAGAGCGTGCACCTCG 1988
QY 359 tgatgagctttgtgaagaggtgagctttttgttcggtgattgtgcaagagagacattata 418
Db 1989 TCATGGAGCTGTGCGCGGGGAGCTCTTCGACGCAATCFCGCCCGGGGGCGAGTACA 2048
QY 419 cagagcgtgcggtaccgttcgcgagaaacgacatcgcggaagtgtgaggagtgtgcatg 478
Db 2049 CGGAGCGCGCGCGCGGAGCTGCTCGCGGCCATCGTGAGATCGTGACACCTGCCACT 2108
QY 479 tcaatggtttatgcataagattttgaagcctgagaaattttgtttgttaacaagaagg 538
Db 2109 CCATGGGGTGTGATGCACCGGACATCAAGCCGAGAACTTCCTGTCTCAGCAAGGAGC 2168
QY 539 aqaattctgacctaaagctattgattgtttgttttattcttctttaaactcgagaga 598
Db 2169 AGGACGCGCGCTCAAGGCCACCGACTTCGGCTCTTCGCTCTTCAAGGAGGGGAGC 2228
QY 599 ggttacagagattgttgaagtccttatttatgctccagaagtgttgaagagaaatt 658
Db 2229 TGCTCAGGGACATCGTGGCAGGCGCTACTACATCGCGCGCGGAGTGTCAAGAGAACT 2288
QY 659 atggaccagagttgatgtgtgagtgctggagttatctctacatcttctgttttggtg 718
Db 2289 ACGGCGCGGAGCGGACATCTGAGCGTGGGGTCTATGCTACATCTTCTCTCGCGGGG 2348
QY 719 ttctcgttttggcgag 736
Db 2349 TGCTCTCTCTTGGGCGAG 2366

RESULT 2
US-08-459-595A-26
; Sequence 26, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 94
; ADDRESS: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
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: Sequence 26, Application US/0845944A
: Patent No. 6121014
: GENERAL INFORMATION:
: APPLICANT: Koziel, Michael G.
:           Desai, Nalini M.
:           Lewis, Kelly S.
:           Kramer, Vance C.
:           Warren, Gregory W.
:           Evola, Stephen V.
:           Crossland, Lyle D.
:           Wright, Martha S.
:           Merlin, Ellis J.
:           Launis, Karen L.
: TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
:                     NUCLEIC ACID CODING SEQUENCE
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,444A
: FILING DATE: 02-Jun-1995
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/951,715
: FILING DATE: 25-SEP-1992
: APPLICATION NUMBER: US 07/772,027
: FILING DATE: 04-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Meligs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: S-18805/PL/CGC1577/CIP/DIV6
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8587
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4162 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1418..1427
: OTHER INFORMATION: /note= "start of mRNA"
: FEATURE:
: NAME/KEY: exon
: LOCATION: 1481..2366
: FEATURE:
: NAME/KEY: intron
: LOCATION: 2367..2451
: FEATURE:
: NAME/KEY: exon
: LOCATION: 2452..2602
: FEATURE:
: NAME/KEY: intron
: LOCATION: 2603..2690
: FEATURE:
: NAME/KEY: exon
: LOCATION: 2691..2804
: FEATURE:
: NAME/KEY: intron

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QY 659 atgaccagaggttggtgagtgctgagtgatccctacacattcttctggtg 718  
 Db 2287 ACGGCCGAGGCGGCACTGCGGCTGCGGCTGCTACATCTTCTCGCCGCG 2346  
 QY 719 ttcttcggttttgagcag 736  
 Db 2347 TGGCTCCCTTCGGCGAG 2364

RESULT 6

US-07-951-715A-20

; Sequence 20, Application US/07951715A

; Patent No. 5625136

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; Zip: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/951,715A

; FILING DATE: 25-SEP-1992

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

; TELEPHONE: (919)541-8615

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1349 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHEICAL: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 3..1226

; OTHER INFORMATION:

; OTHER INFORMATION:

; OTHER INFORMATION:

; OTHER INFORMATION:

; OTHER INFORMATION:

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; OTHER INFORMATION:

; OTHER INFORMATION:

; OTHER INFORMATION:

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; OTHER INFORMATION:

; OTHER INFORMATION:

Query Match 22.1%; Score 225.6; DB 1; Length 1349;  
 Best Local Similarity 60.1%; Pred. No. 3.9e-61;  
 Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 279 gatcatgtcaactttaccggaacacccaaacgttggtaaaacttaagcgacttatgagga 338  
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 Db 65 CAAGCAGAGGCTGCACCTCTGTCATGAGAGCTGTGCGCGGGGGGAGGCTCTTCGACCGCAT 124  
 QY 399 tgttgaaggaggacattatcacagagctggcggggtacacgtgcgcgaagaacatcgcgga 458  
 Db 125 CATCGCCCGGGGCGAGTACACGGAGCGCGCGCGCGGAGCTGCTGGCGCCCATCTGTGCA 184  
 QY 459 agttgagagtggttcattgctgaatggttgcattagagagatttgaagcctgagaattt 518  
 Db 185 GATCGTGCACACCTGCCACTCCATGGGGGTGATCCACCGGGGACATCAAGCCCGGAGACTT 244  
 QY 519 ctgtttgttaacaagaagaggaattctgcacttaaggctattgattttgtttatctgt 578  
 Db 245 CCTGCTGCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTTCGGCCTCTCCGT 304  
 QY 579 tctcttaaacctggagagaggtttcacagagattgttgaagtccttatttatatggtcc 638  
 Db 305 CTCTCTCAAGAGGCGGAGCTGCTCAGGACATCGTGGGCGGAGCGGCTACTACATCGCGCC 364  
 QY 639 agaagtggtgaagagaaattatggaccagaggttgatgtgtgagtgctgagttatcct 698  
 Db 365 CGAGGTGCTCAAGAGGAAGTACGCGCGGAGCGCGACATCTGAGAGGCTCGGCGGTATGCT 424  
 QY 699 ctacatctgtcttgggtgttctctccgttttgggcagagactgaacaagggtgtgctct 758  
 Db 425 CTACATCTCTCCGCGGCTGCTCCTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484  
 QY 759 tgccattgtgagggaggttcctgattttaagagagatccttggtcagagatcacagagag 818  
 Db 485 CGCCATCTCTGAGGCGGAGCTTACCTCTCCAGCGAGGAGGAGGAGGAGGAGGAGGAGG 544  
 QY 819 cgcaagagccttggtaagcagatgttggaaacctgattcaactaaagcgtttgactgtca 878  
 Db 545 AGCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGGCGGCTCAGCGGTT 604  
 QY 879 gcaagttctgtacacaccttgat 902  
 Db 605 CCAGGTCTCAATACCCCATGGAT 628

RESULT 7

US-08-459-448A-20

; Sequence 20, Application US/08459448A

; Patent No. 5859336

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

/note="cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."

;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
;; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
;; NUMBER OF SEQUENCES: 94  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: No. 5859336artis Corporation  
;; STREET: Patent & Trademark Dept., 520 White Plains  
;; STREET: Rd., POB 2005  
;; CITY: Tarrytown  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10591-9005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/459,448A  
;; FILING DATE: 02-JUN-1995  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/951,715  
;; FILING DATE: 25-SEP-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/772,027  
;; FILING DATE: 04-OCT-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Pace, Gary M.  
;; REGISTRATION NUMBER: 40403  
;; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (919)541-8582  
;; TELEFAX: (919)541-8689  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1349 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; HYPOTHEetical: NO  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 3..1226  
;; OTHER INFORMATION: /note= "cDNA sequence for maize  
;; OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as  
;; OTHER INFORMATION: disclosed in Figure 30."  
;; US-08-459-448A-20

Query Match 22.1%; Score 225.6; DB 2; Length 1349;  
Best Local Similarity 60.1%; Pred. No. 3.9e-61;  
Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;  
QY 279 gatcatgcaactttaccggaacacccaaacgttggaacttaagcgacttatgagga 338  
Db 5 GATCATGCACCACTCTCCGGCCAGCAGCCAACTGGTGGGCTCCGGCCGCGTACGAGGA 64  
QY 339 taacgagacgtgcatcttggagagcttggagaggtgagcttttttggtcgat 398  
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Db 125 CATCGCCGGGGCCAGTACACGAGGCGCGCGCGGAGCTGCTGCGCCGCATCGTGA 184  
QY 459 agttgtgagagatgtcatgtcaatgtgtgtatgcatagagatttaagcctgagaattt 518  
Db 185 GATGTGACACCTGCACCTCCATGGGGGGTGTGATGCAACCGGACATCAAGCCGAGAACTT 244  
QY 519 cttgttgtaacaaagagagattctgcacttaaggtctattgtttgtttatctgt 578  
Db 245 CTTGTGCTCAGCAGGAGGAGGAGCGCGGCTCAAGGCCACCGGACTTCGGGCTCTCCGT 304

QY 579 tctotttaaacctggagagaggttttaagagagattgttggaagtccttattatgtctcc 638  
Db 305 CTTCTTCAAGGAGGCGGAGCTGCTCAGGACATGCTCGGACGCGCTACTACATCGCGCC 364  
QY 639 agaagttgtgaagaaaattatgaccagaggtttgatgtgtgagtgctgagagttatct 698  
Db 365 CGAGGTGCTCAAGAGGAGTACGGCCCGGAGCGGACATCTGGAGCGCTCGCGCTCATGCT 424  
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Db 425 CTACATCTTCTCGCGCGGCTGCTCCTCTTCTGGGAGAGACGAGAACGCACTTTCAC 484  
QY 759 tgcatcttgaaggaggttcttgaatttttaagagagacttctggtgcagatatcagagag 818  
Db 485 CGCATCTCTGGAGGCGAGCTTGACCTCTCCAGGAGCCATGCGCCACACATCTCGCGGG 544  
QY 819 cgcaagagccttggagcagagattgttggaacctgattcaactaagcgtttgactgtca 878  
Db 545 AGCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGGTT 604  
QY 879 gcaagttcttgatcaccttgat 902  
Db 605 CCAGGTCTCAATCACCCATGGAT 628

## RESULT 8

US-08-459-595A-20  
; Sequence 20, Application US/08459595A  
; Patent No. 6018104  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, John L.  
; APPLICANT: Dawson, John G.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6018104artis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; STREET: Rd., POB 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,595A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991

22.18; Score 225.6; DB 3; Length 1349;

Best Local Similarity 60.1%; Pred. No. 3.9e-61;  
Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 279 gatcatgtcaactttaccoggaacacccaaacgttgtgaaacttaaaagcagacttatgaga 338  
|||||  
Db 5 GATCATGCCACCACTCTCCGCCAGCCACCAAGTGTGGGCTCCGCCGCGGTACAGGA 64

QY 339 taacagagaccgtgatcttggatggagctttgtgaaggaggtgagcttttggctcgtat 398  
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Db 65 CAAGCAGAGCGTGCACCTCGTCATGGAGCTGGCGCGGGAGGCTTCGACCGCAT 124

QY 399 tttgcaagagagacattatcacagacgtgogcggtaccgtcgcggaacagatogggga 458  
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Db 145 CATGCCCGGGCCAGTACAGGAGCGGGCGCGCGGAGTGTGGCGGCATCGTGCA 184

QY 449 agttgtgaggatgtgtcatgtcaatggtgttatgcataagatttgaagcctgagaattt 518  
|||||  
Db 185 GATCGTGACACCTGCCATCCATGGGGTGATGCACCGGACATCAAGCCCGGAACTT 244

QY 519 cttgtttgtaacaaagaagagaattctgcacttaaggctattgattttggtttatctgt 578  
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Db 245 CCTGCTGCTCAGCAAGGAGGAGACGCGCGGCTCAAGGCGCACCGACTTCGGCTCTCCGT 304

QY 579 tctctttaaacctgagagagatttacagagatttgtgaagctcttatatatgctcc 638  
|||||  
Db 305 CTTCTTCAGGAGGCGGAGCTGCTCAGGACATCGTCGCGAGCGGCTACTATCGCGCC 364

QY 639 agaagtttgaagagaaattatggaccagaggttgtgtgtgtgagctggtgagttatct 698  
|||||  
Db 365 CGAGGTGCTCAAGAGGAACTAGCGCCCGGAGCGCCGACATCTGGAGCGCTCGGCTATGCT 424

QY 699 ctacatcttctgtgtgtgttctctcgttttggcgagagactgaacaaaggtgtgctct 758  
|||||  
Db 425 CTACATCTCTCCGCGCGGCTGCTCCCTTCTGGCAGAGACGAGAAACGGCATCTTCAC 484

QY 759 tgcoattttgaggaggtcttgaatttgaagagagactctgtgtgcagatatcagagag 818  
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Db 485 CGCATCTCTCGAGGCGAGCTTCACTCTCCAGCGAGCCATGGCCACACATCTCGCGGG 544

QY 819 cgcgaagagccttgaagcagatgttggacacctgattcaactaaagcgtttgactctca 878  
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Db 545 AGCCAAGGATCTGCTCAAGAGATGCTCAACATCAACCCCAAGAGCGGCTCAGCGGTT 604

QY 879 gcaagttttgacacaccccttgat 902  
|||||  
Db 605 CCAGGTCTCAATCAACCCATGGAT 628

## RESULT 10

US-08-459-444-20

Sequence 0, Application US/08459444A

Patent No. 6121014

## GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meijs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/OGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8889  
INFORMATION FOR SEQ ID NO: /note= "cdna sequence for maize  
pollen-specific calcium dependent protein kinase gen.  
disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
FEATURE:

NAME/KEY: CDS  
LOCATION: 3..1226  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-08-459-444-20

## Query Match

22.1%; Score 225.6; DB 3; Length 1349;

Best Local Similarity 60.1%; Pred. No. 3.9e-61;

Matches 375; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 279 gatcatgtcaactttaccoggaacacccaaacgttgtgaaacttaaaagcagacttatgaga 338  
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Db 5 GATCATGCCACCACTCTCCGCCAGCCACCAAGTGTGGGCTCCGCCGCGGTACAGGA 64

QY 339 taacagagaccgtgatcttggatggagctttgtgaaggaggtgagcttttggctcgtat 398  
|||||

Db 65 CAAGCAGAGCGTGCACCTCGTCATGGAGCTGTCCGCGGGCGGAGCTCTTCGACCGCAT 124

QY 399 tttgcaagagagacattatcacagagcgtgogcggtaccgtcgcggaacagatogcgga 458  
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Db 125 CATGCCCGGGCCAGTACAGGAGCGGGCGCGGAGCTGCTCGCGGCGCATCTGTCGA 184

QY 459 agttgtgagatgtgtcatgtcaatggtgttatgcataagatttgaagcctgagaattt 518  
|||||

Db 185 GATCGTGACACCTGCCATCCATGGGGTGATGCACCGGACATCAAGCCCGGAACTT 244

QY 519 cttgtttgtaacaaagaagagaattctgcacttaaggctattgattttggtttatctgt 578  
|||||

Db 245 CCTGCTGCTCAGCAAGGAGGAGACGCGCGGCTCAAGGCGCACCGACTTCGGCTCTCCGT 304

QY 579 tctctttaaacctgagagagatttacagagatttgtgaagctcttatatatgctcc 638  
|||||

Db 305 CTTCTTCAGGAGGCGGAGCTGCTCAGGACATCGTCGCGAGCGGCTACTATCGCGCC 364

QY 639 agaagtttgaagagaaattatggaccagaggttgtgtgtgtgagctggtgagttatct 698  
|||||

Db 365 CGAGGTGCTCAAGAGGAACTAGCGCCCGGAGCGCCGACATCTGGAGCGCTCGGCTATGCT 424

QY 699 ctacatcttctgtgtgtgttctctcgttttggcgagagactgaacaaaggtgtgctct 758  
|||||

Db 425 CTACATCTCTCCGCGCGGCTGCTCCCTTCTGGCAGAGACGAGAAACGGCATCTTCAC 484



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QY 759 tgccatttgaagggagtttcttgaatttaagagagatccttggctgcagatatcagagag 818
Db 485 CGCCATCTCGAGGGGAGCTTGACCTCTCCAGCGAGCCATGGCCACACATCTCGCGGG 544
QY 819 cgcaaaagaccttgaagcagagattggaacctgattcaactaagcgtttgactgctca 878
Db 545 AGCCAAGGATCTCGTCAAGAGAGATGCTCACATCAACCCCAAGAGGCGGCTCACGGCGTT 604
QY 879 gcaagttcttgatcaaccttggat 902
Db 605 CCAGGCTCTCAATCAACCCATGGAT 628

RESULT 11
US-09-347-801-3
; Sequence 3, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; EARLIER FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3

Query Match 21.5%; Score 219.8; DB 4; Length 2374;
Best Local Similarity 57.4%; Pred. No. 3.4e-59;
Matches 417; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

QY 206 tagcttgaaatacatctccaagagaaagctccgaaccccgctcgatgtggaagacgtcc 265
Db 796 tcgcgtcaagatcatcgccaaagctaaagatgacaacgccaataatccattgaggatgtc 855
QY 266 gtctgaagtcacgattcgaattcaattaccggaacaccccaacgcttggaacctaaag 325
Db 856 gtagaagaataaaattttgagagcattatccgggacaaataatctgcataattatg 915
QY 326 cgacttatgagataacgagaccgtgcatcttctgtgagagctttgtgaagaggtgagc 385
Db 916 atgcatgtgagatggcctcaatgtctacatgtcatggaattatgtgaggaggagaaat 975
QY 386 ttttggctgattgttgcaga---ggacattatacagagcgtgcggcggtaccgtcg 442
Db 975 tctagacagaattatgacagagcgggagatacacagaggaagatgccaaagcgattg 1035
QY 443 cgagaaacgctcggaagtgtgagatgtcattgtcaatggttgaatgcatagagatt 502
Db 1035 ttgtacagattttgagcgtagtagctctgtcatcttcacgggggtgtagtgcattgtatt 1095
QY 509 tgaagcctgagaattcttctgttgaacaaagagagattctgcactaaaggtattg 562
Db 1096 tgaagccagagaattctctttccacacagggatgaaatgctcccatgaagtgtattg 1155
QY 563 atttgggttactgtctcttctttaaaccctggagaggtttacagagattgttgaagtc 622
Db 1156 atttgggtctctgtatttcattagaccagatgaaagcgttaattatgtattgtggaagt 1215
QY 623 ctattatgctccagaaggttgaagagaattatgaccacagaggttgatgtgtgga 682
Db 1216 catattatgtgcccagaggtttcacacagatcatgattggaagcagacatttggga 1275
QY 683 gtgtggagttatctctacatctgtgttgggttctcctcgttttggggcagagactg 742
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Db 1276 gtatagtgataaagcgtacattctgtctgtgagcagtcgccaattctgggcaagaacag 1335
QY 743 aacaaggtgtggtcttgcctatttgcctatttgcagggaggttcttgaatttaagagagatccttgg 802
Db 1336 aatcaggaatattccgactctgtgtgagagctgatacccaactttgattgattcaacctggc 1395
QY 803 cgcagatatcagagagcgcaaaagacctgtgaagcagatgttgggaacctgattcaacta 862
Db 1396 ctacagtatcagctgaagctaaagatttttgaagagatttctgaacaagagattaccgca 1455
QY 863 agcgtttgactgtcagcaagttctgtacaccttggatcacaccttggatcacagaatgcaaaagga 922
Db 1456 aaagaatgacctgtttcaagcactgactcactcctgtgtgagatgaaacaaagcgaga 1515
QY 923 tcaagct 929
Db 1516 tcccgt 1522

RESULT 12
US-08-464-164-1
; Sequence 1, Application US/08464164
; Patent No. 5614195
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5614195el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,164
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-464-164-1
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Query Match 14.5%; Score 148.2; DB 1; Length 1400;  
Best Local Similarity 52.5%; Pred. No. 8.3e-37;  
Matches 324; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 298 gaacacccaaacgtgtgaaacttaagcgacttatgagataaacgagaccgtgcacttt 357  
Db 151 GATCATCTTAATATCATGAAATATATGAATCTTTGAGGATAAGGATACCTTTATCTT 210

QY 358 gtatgagagcttgtgaagagagcttgggtggatgtgtgcaagagacattat 417  
Db 211 GTTACAGAAATATATACAGAGAGAAATTTTCAATGAATTTATATCGAAAAAGATTC 270

QY 418 acagagcggtgcggtgtgacgtgcgagagacgtgcggaagtgtgagatgtgcatt 477  
Db 271 AGCGAGCGGATCGAGCTGTATAGTACGTCAGGTCATFCGGGTATAAATATATGTCAT 330

QY 478 gtcaatggtgttatgcatagagatttgaagcctgagaatttctgttctaacaagaag 537  
Db 331 CGTAATAAATAATAGTTCATAGAGATTAAAGCCAGAGAAATTTATATAGAGATAAAAA 390

QY 538 gagaattctgcaacttaaggctattgttgggtttgttctgttcttctttaaaccctggag 597  
Db 391 AAGATGCAAAATATACGAATTTATTTGGGTTTATCTACACATTTTGAGCCCAAAAA 450

QY 598 aggtttacagagattgttggaaagtccttattatattgctcccaagaagtgttgaagagaaat 657  
Db 451 AAAATGAAGATATAAATCGGACCGGTACTACATTCGCCCTGAGGTGTCGACGGAACA 510

QY 658 tatgaccagaggtgtgattgtgtgagtgctgagttatctctacatcttctgtgtgtgt 717  
Db 511 TAGCATGAGAAATGCGACGCTGCTGCTACGGGTGTATCTCTATATATCTCTCTGTGT 570

QY 718 gtctccgttttgggagagagactgaacaggtgtggtcttgcctcttgcctgtgagggagtt 777  
Db 571 TGCTCTCCATTTACGGAGCAATGAATTTGAAATTTCTAAAGAAAGTCGAGAAAGGAAAA 630

QY 778 cttgattttaagagagatccttgggtgcagatatcagagagcgcaagagccttgtgaag 837  
Db 631 TTCACCTTCGATTTACACAGTGGCGTAGGTTAGCGAGCCACCAAGAAANTTTAATAGG 690

QY 838 cagatattggaacctgattcaactaagcgtttgactgctcagcaagtcttctgtacacct 897  
Db 691 AAGATGTTAGCATATGATCCCTCAATCGTATATCAGCAAAAGATGATATGATATCA 750

QY 898 tggatacagaatgcaaa 914  
Db 751 TGGATAAAGATACAGA 767

## RESULT 13

US-08-338-057-1  
; Sequence 1, Application US/08338057  
; Patent No. 5795741  
; GENERAL INFORMATION:  
; APPLICANT: Tomley, Fiona M.  
; APPLICANT: Dunn, Paul P. J.  
; APPLICANT: Bumstead, Janene M.  
; APPLICANT: Vermeulen, Arno N.  
; TITLE OF INVENTION: Coccidiosis poultry vaccine  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Organon Teknika Corporation  
; STREET: 1330 Piccard Drive  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: U.S.A.  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: EP 93.309078.9  
FILING DATE: 12-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93.309078.9  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Gormley, Mary E.  
REGISTRATION NUMBER: 34.409  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 258-5200  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1400 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: C-terminal  
ORIGINAL SOURCE:  
ORGANISM: Eimeria maxima  
STRAIN: Houghton  
DEVELOPMENTAL STAGE: sporozoite  
IMMEDIATE SOURCE:  
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII  
CLONE: Em70-1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1368  
US-08-338-057-1

Query Match 14.5%; Score 148.2; DB 1; Length 1400;  
Best Local Similarity 52.5%; Pred. No. 8.3e-37;  
Matches 324; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 298 gaacacccaaacgtgtgaaacttaagcgacttatgagataaacgagaccgtgcacttt 357  
Db 151 GATCATCTTAATATCATGAAATATATGAATCTTTGAGGATAAGGATACCTTTATCTT 210

QY 358 gtatgagagcttgtgaagagagcttgggtggatgtgtgcaagagacattat 417  
Db 211 GTTACAGAAATATATACAGAGAGAAATTTTGAATGAATTTATATCGAAAAAGATTC 270

QY 418 acagagcggtgcggtgtgacgtgcgagagacgtgcggaagtgtgagatgtgcatt 477  
Db 271 AGCGAGCGGATCGAGCTGTATAGTACGTCAGGTCATTCGGGTATAAATATATGTCAT 330

QY 478 gtcaatggtgttatgcatagagatttgaagcctgagaatttctgttctaacaagaag 537  
Db 331 CGTAATAAATAATAGTTCATAGAGATTAAAGCCAGAGAAATTTATATAGAGATAAAAA 390

QY 538 gagaattctgcaacttaaggctattgttgggtttgttctgttctttaaaccctggagag 597  
Db 391 AAGATGCAAAATATACGAATTTATTTGGGTTTATCTACACATTTTGAGCCCAAAAA 450

QY 598 aggtttacagagattgttggaaagtccttattatattgctcccaagaagtgttgaagagaaat 657  
Db 451 AAAATGAAGATATAAATCGGACCGGTACTACATTCGCCCTGAGGTGTCGACGGAACA 510

QY 658 tatgaccagaggtgtgattgtgtgagtgctgagttatctctacatcttctgtgtgtgt 717  
Db 511 TAGCATGAGAAATGCGACGCTGCTGCTACGGGTGTATCTCTATATATCTCTCTGTGT 570

QY 718 gtctccgttttgggagagagactgaacaggtgtggtcttgcctcttgcctgtgagggagtt 777  
Db 571 TGCTCTCCATTTACGGAGCAATGAATTTGAAATTTCTAAAGAAAGTCGAGAAAGGAAAA 630

QY 778 cttgattttaagagagatccttgggtgcagatatcagagagcgcaagagccttgtgaag 837

Db	631	TTCCACCTCGCATTTACACAGTGGCGTAAGGTTAGCGAGCCAGCAAAAGATTAAATTAGG	690
QY	838	cagatgttggaacctgattcaactaagcgtttgaactgctcagcaagtcttgatcacct	897
Db	691	AAGATTAGCATATGTACCTCAATGCGTATATACGAAAGATGCATTAGATCATCCA	750
QY	898	tggatcatcagaatgcaaa	914
Db	751	TGGATAAAAGGTACAGA	767

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RESULT 1A
US-08-668-416-1
; Sequence 1, Application US/08668416
; Patent No. 5843722
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5843722el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,416
; FILING DATE:

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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-668-416-1

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Query Match 14.5%; Score 148.2; DB 2; Length 1400;
Best Local Similarity 52.5%; Pred. No. 8.3e-37;
Matches 324; Conservative 0; Mismatches 293; Indels 0;
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Qy	298	gaacaccaaacgttgaaaccttaaacgcgacttatgagataaacgagacccgtgcactctt	357
Db	151	GATCATCCTAATATCATGAATATATGAATCTCTTCGAGATAAAGGATACTTTATCTT	210
Qy	358	gtgatcgagcttctgaaagaggtgaccttttggctcggtattgttgaagagagacattat	417
Db	211	GTTACAGAAGTATATACGAGGAGGAATATTTGTATGAAATTTAATCGAAAAAGATTTC	270
Qy	418	acagagcgtcggcggctccgtcgcgagaaacgatcgggaagctgtgaggaatgtgcac	477
Db	271	AGCGAGGCGGATCGAGCTCGTATAGTACGTCAGGTCATTCGGGTATAAATATATGCAT	330
Qy	478	gtcaatggtgttagaatagagattggaagccotgagaattottgtttgtcaacaagaag	537
Db	331	CGTAAATAAATAGTTCATAGAGATTTAAAGCCAGAGAATTTATTATGAGAAATAAAAA	390
Qy	538	gagaattctgcacttaaggctattgatttgggtttatcgtctctctttaaacctggagag	597
Db	391	AAAGATCGCAATATACGAATATTGATTTTGGGTATCTACACATTTTGAGCCCCAAAA	450
Qy	598	aggtttacagagattgttgaaatccotattatatatggtccagaagctgttgaaagagaat	657
Db	451	AAAATGAAGGATAAATCGGGACCGCGTACTACATTTGCCCTGAGTGCTGCACGGAACA	510
Qy	658	tatggaccagaggttaatgtgtggaagtctggaattatcctacatcttgtttgttggt	717
Db	511	TACATGAGAAATTCGACGCTCTGCTACGGGGTGTATCCTCTATATCTCTCTCTGTT	570
Qy	718	gttctctcgttttgggcagagactgaacaaggtgtgctcttgccatcttggaggaggt	777
Db	571	TGTCCTCCATTTAACGGAGCAATGAATTTGAAATCTTAAGAAAGTCGAGAAAGGAAA	630
Qy	778	cttgattttaagagagatccttggtcgcagatatacagagagcgaaagagccttbtgaag	837
Db	631	TTCACTTCGATTTACACAGTGGCGTAAGGTTAGCGAGCCAGCAAAAGATTTAATTAGG	690
Qy	838	cagatgttgaaacctgattcaactaagcgtttgaactgctcagcaagtctttgacacct	897
Db	691	AAGATGTTACCATATGTACCCCTCAATGCGGTATATCAGCAAAAGATGCATTAGATATCA	750
Qy	898	tggatacagaatgcaaa	914
Db	751	TGGATAAAAAGTACAGA	767

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RESULT 15
US-08-655-352-10
; Sequence 10, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachtetira W. Poovaiah, Zhihua Liu,
; APPLICANT: Shameekumar Patil, Palsuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klariquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352

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Db 885 CTGCTCAAGAGATACCTTGACATCCATGGGT 915

Search completed: March 3, 2002, 01:28:57  
Job time: 6729 sec

Query Match 13.4%; Score 136.6; DB 3; Length 1776;  
Best Local Similarity 52.1%; Pred. No. 4.1e-33;  
Matches 329; Conservative 0; Mismatches 299; Indels 3; Gaps 1;

QY 275 tcacgatcatgtcaactttaccggaacacccaaactgttgaaacttaaaagcgacttatg 334  
Db 285 TTAAGATCGTCGAAGATGTTCTCCTCATCTCAACGTCATTCATCTCTACGACCTTTGTG 344

QY 335 agataacagagacgctgtcatctgtgatgagctttgtgaagaggtgagctttttgttc 394  
Db 345 AGATCCCTTCGAGGTCATCTCATTTTGGAGCTTTGCTCTGCTGCTGAGCTCTTTGATC 404

QY 395 ggattgttgcaagaggacattatcacagagcggtgcggcggtcacgtgcgcgagaaacgacg 454  
Db 405 GGATTGCTGGGCAAGCAGAGATTAATGAGGCTGGGGCTGCTGCTGCTGAGACAGATAG 464

QY 455 cgsaagtgtagagtgatgtcatgtgcaatggtgttatgcatagagatttgaagcctgaga 514  
Db 465 CTAAGGGGCTAGAGGGGCTACAGGGGCAAGTATAGTTCACAGGGACTTGAACCCAGAGA 524

QY 515 attctgtttgtcaacaagaagagaattctgcacttaagctattgatttgggtttat 574  
Db 525 ACTGCTATTTCTTGACACAGAGTGAAGTACCGGTTGAAGATTATGGATTTTGGGCTGA 584

QY 575 ctgttctctttaacctggagagaggtttacagagattgttggaagtccttatttatgg 634  
Db 585 GTTCTATTGAGGATTTTGCAAATCCAGTGGTGGTTTGGTTGTTCCATAGATTATCTAT 644

QY 635 ctccagaag--tgtgaagagaattatggacgaaggttgatgtgtgagtgctggag 691  
Db 645 CACCAGAAGCAGCTTTCAAGGGAAATATATACACCACTAAAGTATATTTGGTCACTTGGTG 704

QY 692 ttatctctcatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 751  
Db 705 TTATCTTTACATCTCCTCTCTGGGTTACCCACCTTTTCATCGCGCGCTCAATCGAAAA 764

QY 765 agcaacaatgatatttaattggcagttcagtttttgatgagaaaaacctggaaaaacatat 824  
Db 812 cagagagcgaagagacgctgtgaagcagatgtttgaaacctgattcaactaagcgttga 871

QY 825 CTTTCATCGGCAAAACCACTAATTTCCAGTCTCTTTGAAAGTTGATCTTCAACATGAGGCTA 884  
QY 872 ctgctcagaagttcttctgtatcacccttgat 902

FILE DATE: 10/3/2002  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA: 08/323,449  
APPLICATION NUMBER: 08/323,449  
FILING DATE: October 14, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Alan. E.  
REGISTRATION NUMBER: 35,123  
REFERENCE/DOCKET NUMBER: 4630-45000  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1776 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
DESCRIPTION: Tobacco CCAMK cDNA and deduced amino-acid  
FEATURE:  
NAME/KEY: protein-coding sequence (not including  
NAME/KEY: Stop codon)  
LOCATION: nucleotides 20-1570  
US-08-655-352-10

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 23:35:04 ; Search time 1526.19 Seconds  
(without alignments)  
7181.736 Million cell updates/sec

Title: US-08-989-881-1

Perfect score: 1020

Sequence: 1 gttgttaaacacgncagt.....gcttgccgtaatcgtcat 1020

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: em\_estfun:\*
- 2: em\_esthum:\*
- 3: em\_estlin:\*
- 4: em\_estom:\*
- 5: em\_estpl:\*
- 6: em\_estba:\*
- 7: em\_estro:\*
- 8: em\_estov:\*
- 9: em\_htc:\*
- 10: gb\_estl:\*
- 11: gb\_est2:\*
- 12: gb\_htc:\*
- 13: gb\_gss:\*
- 14: em\_gss\_fun:\*
- 15: em\_gss\_hum:\*
- 16: em\_gss\_inv:\*
- 17: em\_gss\_pin:\*
- 18: em\_gss\_pro:\*
- 19: em\_gss\_rod:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424.6	41.6	471	CNS00MGW	AL080606 Arabidops
2	407	39.9	833	BE641223	BE641223 Cri2.2.K0
3	378	37.1	659	AW685409	AW685409 NF029A07N
4	352.4	34.5	594	AI896274	AI896274 EST265717
5	343.2	33.6	656	BE647650	BE647650 NF077A07E
6	339	33.2	350	BE523895	BE523895 M43C3STM
7	336.4	33.0	590	AW443165	AW443165 EST308095
8	333.2	32.7	515	BE435148	BE435148 EST406226
9	333	32.6	455	CNS00ROC	AL087354 Arabidops
10	331.6	32.5	641	AW223685	AW223685 EST300496
11	315	30.9	666	AI054550	AI054550 coau0001F
12	301.6	29.6	657	BE584245	BE584245 6-12E-HA

c	13	299.4	29.4	644	10	BE443407
	14	294	28.8	685	11	BE454189
	15	291.4	28.6	601	10	AW043082
	16	284.6	27.9	731	10	AW256503
	17	282	27.6	501	10	AW931540
	18	279.4	27.4	732	10	AW387032
	19	278.6	27.3	742	11	BE596613
	20	275	27.0	748	11	BE123404
	21	270.6	26.5	582	11	BE616793
	22	267.4	26.2	689	10	AW217987
	23	264.2	25.9	664	10	AW684367
	24	263.4	25.8	608	11	BE140058
	25	263.2	25.8	659	10	AW686132
	26	260.8	25.6	635	10	AW587489
	27	259.8	25.5	742	11	BE1305348
	28	257.6	25.3	758	11	BE365168
	29	257.4	25.2	559	10	BE443788
c	30	257	25.2	687	11	BE600015
	31	255.2	25.0	583	10	AW671890
	32	254.2	24.9	662	10	AW685986
	33	253.6	24.9	718	11	BE126469
	34	253.4	24.8	561	11	BF097701
	35	253	24.8	680	11	BF644542
	36	248.2	24.3	542	10	AW441707
	37	246	24.1	663	11	BF646490
	38	246	24.1	664	11	BF648169
	39	244.6	24.0	759	11	BE365167
	40	242.6	23.8	592	10	AW035209
	41	242.2	23.7	585	11	BE1140443
	42	241.8	23.7	681	11	BE368645
	43	237.4	23.3	652	11	BF646537
	44	235.4	23.1	461	11	BF588161
	45	233.4	22.9	456	11	BF651257

#### ALIGNMENTS

RESULT 1

CNS00MGW	471 bp	DNA	GSS	28-JUN-1999
LOCUS	Arabidopsis thaliana genome survey sequence Sp6 end of BAC F1H12 of			
DEFINITION	IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.			
ACCESSION	AL080606			
VERSION	AL080606.1	GI:5281746		
KEYWORDS	GSS.			
SOURCE	thale cress.			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
AUTHORS	1 (bases 1 to 471)			
JOURNAL	Salanoubat M., Choisme N., Artiguenave F., Brottier P., Wincker P., Samson D., Saurin W., Weissenbach J. and Quetier F.			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 471)			
TITLE	Genoscope.			
JOURNAL	Direct Submission			
FEATURES	Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)			
Source	- Web : www.genoscope.cns.fr)			
Location/Qualifiers	1. .471			
/organism="Arabidopsis thaliana"				
/strain="Columbia"				
/gb_xref="taxon:3702"				
/clone_lib="IGF"				
/clone="F1H12"				
/note="end : Sp6"				
BASE COUNT	132 a	83 c	120 g	136 t
ORIGIN				

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Query Match 41.6%; Score 424.6; DB 13; Length 471;
Best Local Similarity 99.1%; Pred. No. 6e-111;
Matches 427; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 163 ggaatcagctatcttttacagatagagagactcgtgaagcttttagcttgcgaatcaatc 222
Db 1 GGAATCAGCTATCTTTTACAGATAGAGAGACTCGTGAAGCTTTAGCTTGCAATCAATC 60

QY 223 tccaagagaagctccgaacccgcgtcgtgatgtgaagacatccgtcgtgaagtcacgac 282
Db 61 TCCAGAGARAGCTCCGACCCGCGTGTGATGTGAAGACGTCGCTGTGAAGTCACGATC 120

QY 283 atgtcaactttacgggaacacccaaacgcttggtaaaacttaaaagcacttatgagataac 342
Db 121 ATGTCAACTTTACCGGAACACCCAAACGTTGTGAACCTTAAAGGACCTTATGAGATAAC 180

QY 343 gaaacgtgactcttggatggagcttggagagcttggagagcttttttgcgagattgtt 402
Db 181 GAGAACGTGATCTGTGATGAGAGCTTTGTCAAGGAGGTGAGCTTTTGTGATCGGATGTT 240

QY 403 gcaagagacattatcacagagcgtcgccgctaccctcgcgagacgacgacgagagatt 462
Db 241 GCCAGAGAGATATATACAGAGCTGCGCGCTACCGTCGCGAGAACGATCGCGGAGGTT 300

QY 463 gtgaggtgtgctatgctcaatgtgttgcgtatgagagcttgaagcctgagaaattcttg 522
Db 301 GTGAGGATGTCTATGTCATGCTGATGTTGATGATAGAGATTTGAAGCCTGAGATTTCTTG 360

QY 523 ttgcttaacgaagagagaaattctgcaacttaagcgtattgattttgttatctgtctc 582
Db 361 TTGCTTAACGAAGAGAGAAATCTGCACCTTAAGGCTATTGATTGTTTGTATCTGTCCTC 420

QY 583 ttttaaacctgg 593
Db 421 TTTAAACCTGG 431

RESULT 2
BE641223
LOCUS
DEFINITION
CDNA clone Cr12_2_K07 5', mRNA sequence.
ACCESSION
BE641223
VERSION
1
KEYWORDS
EST.
SOURCE
Ceratopteris richardii.
ORGANISM
Ceratopteris richardii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.
1 (bases 1 to 833)
Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
Expressed sequence tags of cDNA clones from a C. richardii library
Unpublished (2000)
Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Cr12_2 row: K column: 07
Seq primer: SP6.
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Location/Qualifiers
1..833
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/db_xref="taxon:49495"
/clone="Cr12_2_K07"
/tissue="Spore"
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/dev_stage="20 hours after germination initiation"
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/note="Vector: pCMWSPORT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."
BASE COUNT 239 a 159 c 210 g 225 t
ORIGIN

Query Match 39.9%; Score 407; DB 10; Length 833;
Best Local Similarity 70.3%; Pred. No. 7.4e-106;
Matches 545; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 144 actcgttcgcgcgaattcgaatcacgtatcttttacagatagagagactcgtgaagc 203
Db 11 ACTTGGTCTGCGTGAATTTGGCATCTTATTATGACAGATCGGAGACTGACGAAGT 70

QY 204 ttttagcttgcgaatcaatctccaagagaaagctccgaacccgcgtcgtatgtgaagacgt 263
Db 71 GCTAGCATGTAAATCTATTTCTAAAGGGAAGCTTTAGGACACCCATAGACATTGGAATGT 130

QY 264 cgcgtggaagtcacgacatcatgtcaactttaccgggaacacccaaacgtttgaaactaa 323
Db 131 TCGAAGAGAGGTGGATATTATGAGACATCTTCTTAAACATCCAAACATTGTGACTTTGGA 190

QY 324 agcgaacttatgagataaacgagacccgtgcactcttgcgtatgagagctttgtgaagaggtga 383
Db 191 AGGGTCTATGAGATGAGAAATGCGATGCACTTTGTTCATGGAACCTATGTGAAGTGGTGA 250

QY 384 gcttttggcgtgattgttgcgaagagacattatcacagagcgtgcgcgcgtaccgtcgc 443
Db 251 ATTGTTTCGATCGCATTTAGCAAGAGGTCTACTACAGGAGAGAGCTGCACGTCGGTTCAT 310

QY 444 gagaacgacgcgcgaagctgtgaggaatgtgcacgtgcgtgcgcgtaccgtcgc 503
Db 311 GCGTACCATCTTGAAGTTCACAGGTTTGCCATAGGATGTTGTCATGACCGCGACCT 370

QY 504 gaagcctgagaatttcttgcgttaacgaagagaaattctgcacttaagcgtattga 563
Db 371 TAAGCCAGAAANNTTCTGTTTGCACAAAGAAAGAAATTCGCCCTTAAGGCTATTGA 430

QY 564 ttttggttatctgtctcttcttaaacctggagagagatttaccagagagattgtggaagtc 623
Db 431 TTTTGGATTATCCATCTTCTTCAACCTCGGAGAGAGTTTACCGAATAGTAGGAAGTCC 490

QY 624 ttattatagctccgaagagctgtggaagagaaattatggaccagagagcttgcgtgag 683
Db 491 ATACTATATGGCACCTGAGTACTGTAAAGAGAGTTATGGCCAGAGTTGATATATGGAG 550

QY 684 tgcgtgagttatctctacatctgtcttgcgttgcgttgcgttgcgttgcgttgcgttgc 743
Db 551 TGCAGGAGTTATATTACATCTTTATGCGGAGTCCCGCTTTTGGCTGAGACCGA 610

QY 744 acaagtggtgcttgcacatcttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 803
Db 611 ACAATTAGTAGCCAGCCCATCTTACGTGGAATGTGGACTTCAACAGAGATCCTTTGGCC 670

QY 804 gcagatcagagagcgaagagccttgcgaagagagcttgcgaagagagcttgcgaagag 863
Db 671 AATGTTTTCAGAAATGCTTAAGCGTATGTCGGGCAAAATGCTTTGGACCATCAAGSCCA 730

QY 864 gcgttgactgctcagcaagcttcttgcaccccttggtacacagatgcgaagaaa 918
Db 731 AAGATTGACAGCTCAACAAGTCTTTCATTCATTCGTCGCTTGTGAAATGCAAGAAA 785

RESULT 3
AW685409
LOCUS
DEFINITION
NF029A07NR1F1000 Modulated root Medicago truncatula cDNA clone
ACCESSION
AW685409
VERSION
AW685409.1
KEYWORDS
EST.
EST 15-JUN-2000
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Db 121 CAGCICGGTGACTCCCAAAATGTTGAAGTGATTCAGATGTCCTATAGCAGGAGTGA 180  
QY 491 tgcataagagattgaagcctgagaattcttctgttctaacagaagagagaattctgcac 550  
Db 181 TGCATCGGACCTCAAGCCTGAAATTTCTGTGTTGAAACAAAGAAAGACAGACCAT 240  
QY 551 ttaagcctattgatttggtttatctctctctctctctctctctctctctctctctctct 610  
Db 241 TGAAGCAATGATTTGGTCTCTCAGTATTTCTTAAAGCCTGGTGAGAGATTTAAACGAA 300  
QY 611 ttattggaagctctattattatgctctccagaaagtggtgaagaaattatgaccagag 670  
Db 301 TTGTGGAGTTCGTACTCAATGCGCCGAGGTGCTGAGAGAGACTATGTCGAGAG 360  
QY 671 tgaatgctggaagctgctgagttatctctctctctctctctctctctctctctctctctct 730  
Db 361 TAGATGCTGGAGTGTGGAGTAATCTCTACATCTTGTATGTTGTTGTTCCACCATTT 420  
QY 731 ggcagagactgaacaagtggtgctcttgcctcttgcctcttgcctcttgcctcttgcct 790  
Db 421 GGCAGAACTGAACAAAGAGTTGCACAGCAATCAITGCTTCTGTGTGAAATTTAA 480  
QY 791 gagatcttggtgcagatatacagagagcgcaagagccttgcagagagagagagagag 850  
Db 481 GGCAGCCTTGGCCTAAGTATCCGACAATGCAAAAGACCTTGTGAAGAGATGCTTA 540  
QY 851 ctgattcaactaagcgttgcagctgcagcaagcttgcagcaagcttgcagcaagcttgcag 904  
Db 541 CTGATCTAGCCGAGGCTACTGCTCAAAAGTTCTAGATCATCCTCGATAC 594

RESULT 5  
BF647650  
LOCUS BF647650 656 bp mRNA EST 20-DEC-2000  
DEFINITION NF077A07EC1F052 Elicited cell culture Medicago truncatula cDNA  
clone NF077A07EC 5', mRNA sequence.  
ACCESSION BF647650  
VERSION BF647650.1 GI:11912780  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
REFERENCE 1 (bases 1 to 656)  
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation -  
Center for Medicago Genomics Research  
Unpublished (2000)  
Contact: Dixon RA  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7302  
Fax: 580 221 7380  
Email: radixon@noble.org  
Insert Length: 656 Std Error: 0.00  
Plate: 077 row: A column: 07  
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/note="Cells were induced six days after subculture"  
/note="Vector: Lambda Zap; Cells were induced with yeast  
cell wall extracts equivalent to 50ug/ml glucose in the

final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation.

BASE COUNT 206 a 96 c 162 g 188 t 4 others  
ORIGIN

Query Match 33.6%; Score 343.2; DB 11; Length 656;  
Best Local Similarity 72.5%; Pred. No. 1.4e-87;  
Matches 469; Conservative 0; Mismatches 176; Indels 2; Gaps 2;

QY 113 aatcagcagcaagctcatcttagcagcagaactcgtgcgcgcgaattcgggaatcac-g 171  
Db 8 AGATATTACAAATAGCAATAGGATTTAGGAGAGAAATAGGAGAGAGAAATTTGGATTAACNG 67  
QY 172 tatctgttacagatagagagact-cgtgaagcttttagcttgcacatcaatctccaaagag 230  
Db 68 TATTTATGTAAGATAGAGAAACNGGAGAGAAATAGCTTGTAAATCGATTTCAAAGGA 127  
QY 231 aaagctccgaacccgcgtgagtggaacagctccgtcgtgaagtccacatcatgtcaac 290  
Db 128 TAAGCTAAAGAACAGCGATTGATTTGAAGATGTTAGAAGAGAGGTTTGAATTAAGAGCA 187  
QY 291 ttaccggaacaccccaaacgcttgtaaaccttaagcgacttatgagagataaacgagaccgt 350  
Db 188 TTACCTTAACATCCTTAATATTGTTAGCTTGAAGGATACATTATGAAGATGATGATAATGT 247  
QY 351 gcatcttgatgagagctttgtgaagagagtgagctttttgtgcgattgtgcagagag 410  
Db 248 TCACTGTGTATGAGAGCTTTGTGAAGTGGTGAGCTTTTGTATCGGATTTGTCTAAGGG 307  
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Db 308 ACAATTATACGACGCGCCCGCGGCTGGTTAGACCATCGTTCAAGTTCTTCAGAT 367  
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Db 368 GTGCCACGAAATGTTGTGATGCATCGGATCTCAACCCGAGAACTTTTGTGTTGCAA 427  
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Db 428 CAAGAAGGAACATCACTTTGAAAGCTATTGACTTTGGTTGCTAAATACCTTTAAACC 487  
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Db 488 AGTGATATAATTTAACGAGATAGTTGGGAGTCCATATACATGCCCTCAAGTATTGAA 547  
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QY 711 ttgtgtgttctccctgtttggcagagactgaacaggtgtgtgctc 757  
Db 608 TTGTGGNATCCCTCTTTTGGGCANAACTGAGCAGGGGAATGCTC 654

RESULT 6  
BE523895  
LOCUS BE523895 350 bp mRNA EST 19-MAR-2001  
DEFINITION M43C3STM Arabidopsis developing seed Arabidopsis thaliana cDNA  
clone M43C3 5', mRNA sequence.  
ACCESSION BE523895  
VERSION BE523895.1 GI:9781873  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 350)  
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de  
Ibarra, O., Jaworski, J.G., Ohlrogge, J. and Bening, C.  
A new set of Arabidopsis expressed sequence tags from developing



seeds. The metabolic pathway from carbohydrates to seed oil  
Plant Physiol. 124 (4), 1582-1594 (2000)

JOURNAL  
MEDLINE

20567808  
Contact: Benning, C  
Dept. of Biochemistry & Molecular Biology  
Michigan State University  
224 Biochemistry, Michigan State University, East Lansing, MI 48824  
, USA

Tel: 517 355 1609  
Fax: 517 353 9334

Email: benning@msu.edu  
Michigan State University DNA Sequencing Facility Arabidopsis  
Biological Resource Center, The Ohio State University, 309 Botany &  
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:  
6142922603 TEL: 6142923371.

## FEATURES

source

Location/Qualifiers  
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Site\_1: EcoRI; Site\_2: XhoII"

BASE COUNT

95 a 69 c 101 g 85 t

ORIGIN

Query Match 33.2%; Score 339; DB 10; Length 350;

Best Local Similarity 98.6%; Pred. No. 2e-86; Mismatches 5; Indels 0; Gaps 0;

Matches 342; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 151 cgcggcaattcggaatcagctatctttgtacagatagagagactcgtgaagcttttagct 210

Db 4 CGAGGCGAATTCGGAATCAGTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCT 63

QY 211 tcaaatcaatctccaaagaaagctccgaacccgcgtgatgtgaaagcgtccgtcgt 270

Db 64 TCGAAATCAATCTCCAAAGAAAGCTCCGAAACCGCGTGCATGTGGAAGACGTCGCTCGT 123

QY 271 gaagtcacatcatgtcaacttacggaacacccaaagctgtgaaacttaagagact 330

Db 124 GAGTCACCATCATGTCTCACTTTACCGACACCCCAACCTTTGTGAACCTTAAAGCGACT 183

QY 331 tatgagataacagacgcgtgcattctgtgatgagcttttgtgaaaggaggtgagctttt 390

Db 184 TATGAGGATAACGAGAACGTGTCATCTTGTGATGAGCTTTGTGAAGGAGTGAGCTTTT 243

QY 391 ggtcgattgttgaagagagacattatacagagcgtgcgagcgtaccgtcgagagacg 450

Db 244 GATCGGATGTTGCCAGAGAGACATTTACAGACGCGTGCAGCGCTACCGTCGCGAGAACG 303

QY 451 atcgcggaagtgtgaggtgtgcatgtcaatggtgttatgcatag 497

Db 304 ATCGCGGAGGTTGTGAGGATGTCTCATGTGCAATGGTGTATGATAGTAG 350

RESULT 7

AW443165

LOCUS

DEFINITION EST308095 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA

clone cLET43E12 5', mRNA sequence.

ACCESSION AW443165

VERSION AW443165.1

KEYWORDS GI:6985347

SOURCE EST.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

## REFERENCE

AUTHORS

Lycopersicon.

1 (bases 1 to 590)

D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,

Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowman,C.L.,

Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni

,J.J. and Martin,G.B.

Generation of ESTs from tomato callus (mixed elicitor)

Unpublished (1999)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1..590

/organism="Lycopersicon esculentum"

/cultivar="Rio Grande PtoR"

/db\_xref="taxon:4081"

/clone="cLET43E12"

/clone\_lib="tomato mixed elicitor, BTI"

/tissue\_type="leaf"

/dev\_stage="4-6 week old plants"

/lab\_host="XLI-Blue MRF"

/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:

XhoI; cLET - Inoculated with a variety of disease response

elicitors. Plants exposed to 2,6 dichloroisonicotinic

acid, BTH, jasmonic acid, ethylene, fenthion, EIX, EcoRI

okadaic acid, or systemin prior to tissue harvest.

site was destroyed during cloning."

BASE COUNT 164 a 100 c 153 g 173 t

ORIGIN

Query Match 33.0%; Score 336.4; DB 10; Length 590;

Best Local Similarity 73.4%; Pred. No. 1.2e-85;

Matches 430; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 329 cttatagagataacgagacgcgtgcattctgtgatgagctttgtgaaggaggtgagcttt 388

Db 5 CGTGTGAGGATGAAATGCGGGTTCATTGTGTGATGGAACCTATGTGAAGGTGGTGAGCTGT 64

QY 389 ttggtcggattgttgaaggagacattatacagagcgtgcggtaccgtcgcgagaa 448

Db 65 TTGATGAGATCGTGTGAGGGGCGCATTTACTGACAGCAGCTGCTGTTCACGGA 124

QY 449 cgatcgcggaagtgtgaggtgtgcatgtcaatggtgttatgcatagagatttgagc 508

Db 125 CGATTTGAGAGTGTGCAGCTTTTGCACAAACATGGAGTGATTTCATAGAGATTGGAAC 184

QY 509 ctgagaatttctgttgcatacaagaagagaattctgcacttaagcttatgatttg 568

Db 185 CCAGAACTTTTGTGTGTAATAAGAAAGAAATTCACCTCTTAAAGCAATGATTGTG 244

QY 569 gttattctgtctctttaaaccctggagagaggtttacagagattgttgggaagctctatt 628

Db 245 GCITGTCAATCTTCTTCAAGCCAGGTGAGAGTTTCCGAAATAGTTGGAAGTCCATATT 304

QY 629 atatgctccagaagtgttgaagagaaattatgaccagaggttgatgttgagagtgctg 688

Db 305 ATATGGCTCTGAGGTGCTCAAAACGAAACTATGACAGAAATAGATATATGAGAGTCAG 364

QY 689 gattatcctctacatcttctgtgtgtgtctcctcgttttgggagagagactgaacaag 748

Db 365 GAGTCATTTTATATATTTTGTATGTGGGTTCCTCCCTTTTGGGCTGATCTGACACAG 424

QY 749 gtgtggtcttgcctatcttgaggggagttcttatttaagagagagatccttgcgcaga 808

Db 425 GTGTGCCCAAGCCATTTTACGTGGGGCAATTGATTTCAAACGGGAACCTGGGCTAGTA 484

QY 809 taccagagagcgaagagcctgttgagcagagatgttggaaacctgattcaactaagcgtt 868

Db 485 TTTCAGAAAGGTGCTAAATAATCTTTGTCAGGCAAAATGTTAGAGGCGCAGATCCAAAGCTTCGAC 544

```

QY 869 tgaactgcagcaagtcttctgatacccttgatcacagaaatgcaaa 914
DB 545 TGTCTGCAAGCAAGTCTGATGAACACCCCTTGCTTCAAAATGCTAA 590

RESULT 8
LOCUS BE435148 515 bp mRNA EST 18-MAY-2001
DEFINITION EST406226 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
clone cLEG25A6, mRNA sequence.
ACCESSION BE435148
VERSION BE435148.1 GI:9432991
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 515)
AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,I.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
TITLE Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished (2000)
COMMENT Contact: CUGI
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Source
1..515
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG25A6"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/Note="Vector: pBluescriptSKMuadapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 139 a 74 c 142 g 160 t
ORIGIN
Query Match 32.7%; Score 333.2; DB 10; Length 515;
Best Local Similarity 78.0%; Pred. No. 1e-84;
Matches 401; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 304 ccaaacgttgtgaaacttaagcacttatgagataaacgagaccgtgcacttgtgatg 363
DB 2 CCAAAATATGTGAAGTGTGAGAGCTACTATGGAAGATAATGAAGCAGTCTCATCTGTATG 61

QY 364 gactttgtgaaggaggtgagctttttgttcgagattgttgcaagaggacattatacagag 423
DB 62 GAGTTATGTGAAGGTGGGGAGTGTGTTGATAGAATTGTAGTAGAGGGCATTCACAGTGAA 121

QY 424 cgtgcggcgctaccgtcgcgagaagatcgcggaagtgtgagaggtgtgtcatgtcaat 493
DB 122 AGAGCTCAGCTGGGTGTCGCAAACTGTGACAGAAAGTTGTAAGGATGTGTCATGTCAAT 181

QY 484 ggtgttatgcatagagatttgagcctgagaatttctgtttgtctaacagaaggagaat 543
DB 182 GGGGTATGATAGAGACTTGAACCTGACAAATTTTCGTTGCTTAATAAGAAAGACAT 241

QY 544 tctgcacttaaggctatttgatttggtttatctgttctctttaaacttgagagaggttt 603

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DB 242 TCTGCTCTTAAGCCATCGATTTTGCCCTATCTGCTTTTCAAGCTGGTGAAGATTTC 301
QY 604 acagagatttgtggaagtccttattatatgtgtccagaagtgttgagaagaaattatgga 663
DB 302 TCTGAGATTGTGGGAAGTCCATACTACATGGCCACAGAGGTGTGAAGCGGAATTATGGA 361
QY 664 ccagaggttgatgtgtggaagtgcaggttaccctacatcttctgtgtgtgttct 723
DB 362 CCAGAAGTTGATATTGGAGTGTGCTGTCATCCTTTATATTGTATGTGGGGTTCCT 421
QY 724 ccgttttgggcagagactgaacaagtgtggtcttggccatcttggagggaggtcttctgat 783
DB 422 CCATTTTGGCTCAAACTGACACAGAGTGTCTCTTTCAATTTTAAGGGAGTGATAGAT 481
QY 784 tttaagagagactccttggtgcagatatcagaga 817
DB 482 TTCAGAGAGGAACCATGGCTCAAGTCTCTGAAA 515

RESULT 9
CNS00ROC 455 bp DNA GSS 28-JUN-1999
LOCUS Arabidopsis thaliana genome survey sequence SP6 end of BAC F14D16
DEFINITION of IGF library from strain Columbia of Arabidopsis thaliana,
genomic survey sequence.
ACCESSION AL087354
VERSION AL087354.1 GI:5288494
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 455)
AUTHORS Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 455)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
FEATURES
Location/Qualifiers
1..455
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="IGF"
/clone="F14D16"
/Note="end : SP6"
BASE COUNT 129 a 117 c 81 g 128 t
ORIGIN
Query Match 32.6%; Score 333; DB 13; Length 455;
Best Local Similarity 84.3%; Pred. No. 1.1e-84;
Matches 375; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 95 ccatggttaatacaactcagatcagcgacaagtacatctcttagaagaaactcgtcgcg 154
DB 445 CTATGAGCAATCAAACTCAGATCAGGCACAAATACATCTTAGTCTGTAATTAGTCGAG 386
QY 155 gcaaatcggaaatcaactgtatctttgtacagatagagagactcgtgaagcttagcttga 214
DB 385 GCGAATTTCGGAATCAGTCACTTACCTCTGCTACTGATCGTGAACCCACGAGCTTTAGCTTGA 326
QY 215 aatcaatctccaagagaaaaagctccgaacccgtcgatgtggaagacgtccgtcggaag 274
DB 325 AATCGATTTCAAAGCGNAAGCTTCGACACAGCTGTGCTATATCGAAGACGCTTCGTCGAGG 266
QY 275 tcacgatcatgtcaactttaccgcggaacacccaaacgttgtgaaacttaaacgacttatg 334

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Db 265 TAGCGATTATGCTTACTTGAGCATCCAAAGTAGTAAAGCTAAGCTAGTAG 206
Qy 335 aggaataacgagaccgtgcatcttgatggagcttttgaaggagggtgagctttttgtgc 394
Db 205 AGGATAACGAGAACGTGCATCTGTTATGGAGCTTGTGGAAGGAGGTGAGCTTTTGATC 146
Qy 395 ggattgttgaaggagcattatcacagagctgcggcggtaccgctgcggagaacgctgc 454
Db 145 GGATTGTGTGAGAGGACATTACACGGAGCGTGTCTGCTGAGCTGTTGCGGAGAACGATTG 86
Qy 455 cggagttgtgagatgtgcatgctcaatgtgttatgcatagagatttgaagcctaaga 514
Db 85 CTGAGTTGTGATGATGCTGCTCACTTAAGGAGTATGCAATCGAGATTGAAACCTGAGA 26
Qy 515 attctgtttgtctaacaagaagga 539
Db 25 ATTCTCTGTTGCTTAATAAAAAAGGA 1

RESULT 10
AW223685 641 bp mRNA EST 18-MAY-2001
LOCUS EST300496 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
DEFINITION clone cLEN12D10, mRNA sequence.
ACCESSION AW223685
VERSION AW223685.1 GI:5535369
KEYWORDS tomato.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 641)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Renning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..641
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEN12D10"
/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stages="red ripe (7-20 days post-breaker)"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
181 a 111 c 162 g 187 t

BASE COUNT 181 a 111 c 162 g 187 t
ORIGIN

Query Match 32.5%; Score 331.6; DB 10; Length 641;
Best Local Similarity 73.9%; Pred. No. 3e-84;
Matches 421; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

Qy 348 cgtgcactcttgatggagctttgtgaaggagggtgagctttttgttcggtatgttgcaag 407
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Db 7 CGTCAATTGGTGAATGAACATATGTAAGAGTGGTGAGCTGTTTGTATAGATCGTTGCTAG 66
Qy 408 aggaattatcacagagcgtgcggcggtaccgctgcggagaacgacgcgggaagtgtgtgag 467
Db 67 GGGGCATTATCTAAGCAGCAGCTGCTGCTGTTTACACGGACGATTGTGGAGTTGTGCA 126
Qy 468 gatgtgcatgccaatgggttatgcatagagatttgaagcctgagaattttctttttgc 527
Db 127 GCTTTGTCCAAACATGGAGTGATTTCATAGAGATTGAAGCCCGAGAACTTTTGTGTTGC 186
Qy 528 taacaagaagagaaattctgcacttaagctattgatttggtttatctgtctctttaa 587
Db 187 TAAATGAAGAGAAATTCACCTCTTAAAGCAATTTGATTTTGGCTTGTCAATCTCTTCAA 246
Qy 588 acctggagagaggtttcacagagatttgggaagtccttatttatatggtccagaagtgtt 647
Db 247 GCCAGGTGAGAAGTTCTCCGAAATAGTTGGAAGTCCATATATATGCTCCTGAGTGTCT 306
Qy 648 gaagagaaattatgagaccagaggttgatgtggagtgctggagttatcctctacattt 707
Db 307 CAACGAAACTATGGACCAGAAATAGATATATGGAAGTGCAGAGATCATTTTATATATTTT 366
Qy 708 gctttgtggttctcctcgcttttggcgagagactgaacaagtggtgctcttgcctatt 767
Db 367 GTTATGTGGGTTCTCTCCCTTTTGGGCTGAATCTGAAACAAGGTGTGCCCAAGCCATT 426
Qy 768 gaggggagttcttattttaagagagatccttggctgcagatatcagagagcgcaagag 827
Db 427 ACGTGGGCAATTGATTTCAAACGGGAACCCCTGGCTAGTATTTCAGAAGGTGCTTAAAAA 486
Qy 828 ctttgaagcagatgttggaaacctgattcaactaagcgttggactgtcagcaagtct 887
Db 487 TCTTGTCAAGGCAATGTTAGAGGCAGATCCAAAGCTTCGACTGTCTGCAACCAAGTACT 546
Qy 888 tgatcaccttggtacacagaatgcaaaagaa 917
Db 547 TGAACACCTTGGCTTCAAAATGCTTAAGAA 576

RESULT 11
AI054550 666 bp mRNA EST 16-JUL-1998
LOCUS coau0001F17 Cotton Boll Abscission Zone cDNA Library Gossypium
DEFINITION hirsutum cDNA clone coau0001F17 5', mRNA sequence.
ACCESSION AI054550
VERSION AI054550.1 GI:3325664
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; euroids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 666)
Wan,C.-H., Yu,Y., Sasinowski,M. and Wing,R.A.
Cotton EST Database: Sequence Analysis of 2000 cDNA Clones from an
Abscission Zone Library
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: SP030 (AACAGCTATGACCATGATTA)
High quality sequence stop: 282.
Location/Qualifiers
1..666
/organism="Gossypium hirsutum"
/db_xref="taxon:3635"
/clone="coau0001F17"
/clone_lib="Cotton Boll Abscission Zone cDNA Library"

FEATURES
Source
1..666
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF097G08LF"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/notes="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
BASE COUNT      203 a  92 c  164 g  224 t
ORIGIN

Query Match      28.8%; Score 294; DB 11; Length 685;
Best Local Similarity 66.4%; Pred. No. 1.9e-73;
Matches 437; Conservative 0; Mismatches 220; Indels 1; Gaps 1;

QY 291 ttaccggaacacccaacgctgtgaaacttaagcgacttatgagataacgagacct 350
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 TTTGAGTGTCAACCAAAATATTGTTGAATTTAAAGGAGCTTATGAGGATAGGAATTCAGT 60

QY 351 gcaatctgtatgagagcttctggaaggagctgagc-ttttggctggattgttgaagag 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db -61 TCATGTGTGTTGAAGACTTGTGCTGTGTGTAACNTTTTGTATGAGATCATTTGCTAAAG 120

QY 410 gacattatacagagcgtgcggcggtaccgtgcgagaaacgatcgcggaagtttgagga 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GACATATAGTGAAGAGCTGTCTCTATTTGTAGACAGATGTTTAATGTGTTAATA 180

QY 470 tbtgtcatgtaagtgttatgcataagatttgaagcctgagaaattcttctgtttgcta 529
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTTGTCTATTTATGGAGTTATGCATAGGGATCTGAACACAGAGAATTTCTTTGTGGCTA 240

QY 530 acaagaagagaaattctgcacttaagctattgatttggatttcttctcttaaac 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GTAAGATGAATGCACTCTTAAGGCTACTGATTTGTTGTTGCTGTTTCAATGAAG 300

QY 590 ctggagagaggtttacagagattgttggagctctattatatggctccagaaagtgtga 649
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AAGGAAGGTGATCGCGATATAGTCGGAAGTCTTATTTATGTTGCTCAGAGTTCCTC 360

QY 650 agagaaattatgaccagaggttgatgtgtgagtgctgaggtatctctacattctgc 709
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GTCGTAGATCGCGGAAGAAATAGATATATGAGTGCAGAGTTATCTATATATCTTAC 420

QY 710 ttgtgtgttctccgttttggcagacacgaacaaagtgtggtcttggcattctga 769
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 TTAGTGTGTCCTCCATTTTGGCTGTGACACTGAAAGGGAATTTTGTATGCAATATGG 480

QY 770 gggaggtcttatttaagagagatccttggctgcagatacagagagcgcaaaagacc 829
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 AAGGTCTATTTGATTTGAAAGTGAACCGTGGCTTAAATTTTCAGACAGCGCCAGGATC 540

QY 830 ttgtgaagcagatgttgaaacctgatttaacaaagcgtttgactgctcgaagttcttg 889
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 TTGTCGTAATATGCTTATACAGGACCCGAAAGAACGCAATCCCGTGCACAGGTTCTAG 600

QY 890 atacccttggatacagaagtcaaaagaaagatcaagcttatcatcaccgtcgaact 947
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AGCATCTTGGATTAAGATGTATGCTTCTGATANGCAATAGACAGTGCAGTTCT 658

RESULT 15
AW043082
LOCUS
DEFINITION
ST29B03 Pine Triplex shoot tip library Pinus taeda cDNA clone
ST29B03, mRNA sequence.
ACCESSION
AW043082
VERSION
AW043082.1 GI:5903611
KEYWORDS
EST,
loblolly pine.
SOURCE
Pinus taeda
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

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REFERENCE
AUTHORS      Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.
TITLE        The Pine Gene Discovery Project
JOURNAL      Unpublished (1999)
COMMENT      Contact: Ross Whetten
              Forest Biotechnology Group
              North Carolina State University
              Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
              ,NC, 27695-8008
              Tel: 919-515-7800
              Fax: 919-515-7801
              Email: rosswhetten@unity.ncsu.edu
              Seq primer: 5' lambda Triplex2 Sequencing Primer.
              Location/Qualifiers
                1..601
                  /organism="Pinus taeda"
                  /db_xref="taxon:3352"
                  /clone="ST29B03"
                  /clone_lib="Pine Triplex shoot tip library"
                  /lab_host="E. coli BM25.8"
                  /note="Organ: shoot tips; Vector: Lambda Triplex; Site_1:
                  SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from
                  apex) were collected during the spring, frozen and used
                  for mRNA isolation. The SMART-PCR method (Clontech) was
                  used to prepare a library from 1 ug total RNA, using the
                  lambda triplex vector. Plasmid subclones in pTriplex were
                  recovered by cre-lox excision in E. coli strain BM25.8 and
                  sequenced from the 5' end."
BASE COUNT   164 a  117 c  167 g  149 t
ORIGIN

Query Match      28.6%; Score 291.4; DB 10; Length 601;
Best Local Similarity 69.7%; Pred. No. 1e-72;
Matches 405; Conservative 0; Mismatches 175; Indels 1; Gaps 1;

QY 136 ggaacagaactcgtgcgcgaattcgaatacagctatctttgtacacataagaagact 195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 17 GGAAGAGAGCTCGGAGGGGTGAGTTCGGCATTTACTCTTTGTACTGACAGGAGACT 76

QY 196 cgtgaagctttagcttgcaaatcaattctcaagagaagctccgaaccccgctcgatgtg 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 GAAGAAATGCTTGCCTGCAAGTCTATTTCGAAGCGGAAGCTCAGAACACGATAGATAC 136

QY 256 gaagacgtccgttggaatcagatcattgtcaactttaccggaaacacccaaactgttg 315
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 GAGGATGTGAGCGGAGAGTAGCTATATATGAACAATTTGCTCAGCATCCGAACATTGT 196

QY 316 aaacttaagcgacttatgagataacgagacgctgcatcttgtgtgagctttgtgaa 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 ACCTTGAAGCCACGTTACGAGGACGACAGCTGTGTCATCTGTCATGAGGCTCTCGAG 256

QY 376 ggaagtgaacttttggctggattgttgcaaggagcattatcacagcgtgogggcgt 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 GGTGGAGAGCTATTTCACAGGATCGTGTCTAGAGGCGATTACAGCGCGTGCGGGGCT 316

QY 436 accgtgcgagaaacgatcgcggaagtgtgagagatgtgcatgtcaataggtttatgat 495
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 GCTGTACAGCTACTATTGTTGAAGTGTTCAGATGTGTCACAAAACCGGGTGATGAT 376

QY 496 agagatttgaagcctgagaattcttggctgaacagaagagaattctgcacttaag 555
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 CGGACCTCAACCTGAGAGATTTCTGTTGGGATATAAAAGAGAGATTCACCTCTGAAG 436

QY 556 gctattgatttgggtttatctgtctcttaaacctggagagaggtttacagagattgtt 615
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 437 GCTATTGATTTCGGTCTTTCTGTGTTCTTTAAAGCCAGGCGAGGANTTTCTGAAATAATG 496

QY 616 ggaagtcctattatattggctccagaaggtgtgaagagaaattatggaccagagttgat 675
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 497 GGTAGCCCATATATACATGGCAAAAGTCTTGAAAGCNGAAGTATGAGCAAAAGGTGAT 556

QY 676 gtgtggagtgctggagttatctctacatcttctgtgtgtg 716

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Db 557 -TTGGAGTGC AAGGTCATCCGTCANTTTATGNGTGGGG 596

Search Completed: March 3, 2002, 00:02:31  
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